

*Jordan*

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/511,096  
Source: PCT  
Date Processed by STIC: 06/15/2005

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PCT

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/511,096

DATE: 06/15/2005

TIME: 16:10:17

Input Set : A:\US10511096-seq list.txt  
 Output Set: N:\CRF4\06152005\J511096.raw

3 <110> APPLICANT: Evotec NeuroSciences GmbH  
 5 <120> TITLE OF INVENTION: Diagnostic and therapeutic use of a Golgi protein for  
 6 neurodegenerative diseases  
 8 <130> FILE REFERENCE: P67813US1  
**C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/511,096**  
**C--> 11 <141> CURRENT FILING DATE: 2004-10-14**  
 13 <160> NUMBER OF SEQ ID NOS: 27  
 15 <170> SOFTWARE: PatentIn Ver. 2.1  
 17 <210> SEQ ID NO: 1  
 18 <211> LENGTH: 36  
 19 <212> TYPE: DNA  
 20 <213> ORGANISM: Artificial Sequence  
 22 <220> FEATURE:  
 23 <223> OTHER INFORMATION: Description of Artificial Sequence: golgin-245  
 24 cDNA fragment  
 26 <400> SEQUENCE: 1  
 27 agttaagttt ctttgtaaaa cactgatttt ttctcc 36  
 30 <210> SEQ ID NO: 2  
 31 <211> LENGTH: 2228  
 32 <212> TYPE: PRT  
 33 <213> ORGANISM: Homo sapiens  
 35 <400> SEQUENCE: 2  
 36 Met Phe Lys Lys Leu Lys Gln Lys Ile Ser Glu Glu Gln Gln Gln Leu  
 37 1 5 10 15  
 39 Gln Gln Ala Leu Ala Pro Ala Gln Ala Ser Ser Asn Ser Ser Thr Pro  
 40 20 25 30  
 42 Thr Arg Met Arg Ser Arg Thr Ser Ser Phe Thr Glu Gln Leu Asp Glu  
 43 35 40 45  
 45 Gly Thr Pro Asn Arg Glu Ser Gly Asp Thr Gln Ser Phe Ala Gln Lys  
 46 50 55 60  
 48 Leu Gln Leu Arg Val Pro Ser Val Glu Ser Leu Phe Arg Ser Pro Ile  
 49 65 70 75 80  
 51 Lys Glu Ser Leu Phe Arg Ser Ser Ser Lys Glu Ser Leu Val Arg Thr  
 52 85 90 95  
 54 Ser Ser Arg Glu Ser Leu Asn Arg Leu Asp Leu Asp Ser Ser Thr Ala  
 55 100 105 110  
 57 Ser Phe Asp Pro Pro Ser Asp Met Asp Ser Glu Ala Glu Asp Leu Val  
 58 115 120 125  
 60 Gly Asn Ser Asp Ser Leu Asn Lys Glu Gln Leu Ile Gln Arg Leu Arg  
 61 130 135 140  
 63 Arg Met Glu Arg Ser Leu Ser Ser Tyr Arg Gly Lys Tyr Ser Glu Leu  
 64 145 150 155 160  
 66 Val Thr Ala Tyr Gln Met Leu Gln Arg Glu Lys Lys Leu Gln Gly

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67	165	170	175	
69	Ile Leu Ser Gln Ser Gln Asp Lys Ser	Leu Arg Arg Ile Ala Glu	Leu	
70	180	185	190	
72	Arg Glu Glu Leu Gln Met Asp Gln Gln Ala Lys Lys His	Leu Gln Glu		
73	195	200	205	
75	Glu Phe Asp Ala Ser Leu Glu Glu Lys Asp Gln Tyr Ile Ser Val Leu			
76	210	215	220	
78	Gln Thr Gln Val Ser Leu Leu Lys Gln Arg Leu Arg Asn Gly Pro Met			
79	225	230	235	240
81	Asn Val Asp Val Leu Lys Pro Leu Pro Gln Leu Glu Pro Gln Ala Glu			
82	245	250	255	
84	Val Phe Thr Lys Glu Glu Asn Pro Glu Ser Asp Gly Glu Pro Val Val			
85	260	265	270	
87	Glu Asp Gly Thr Ser Val Lys Thr Leu Glu Thr Leu Gln Gln Arg Val			
88	275	280	285	
90	Lys Arg Gln Glu Asn Leu Leu Lys Arg Cys Lys Glu Thr Ile Gln Ser			
91	290	295	300	
93	His Lys Glu Gln Cys Thr Leu Leu Thr Ser Glu Lys Glu Ala Leu Gln			
94	305	310	315	320
96	Glu Gln Leu Asp Glu Arg Leu Gln Glu Leu Glu Lys Ile Lys Asp Leu			
97	325	330	335	
99	His Met Ala Glu Lys Thr Lys Leu Ile Thr Gln Leu Arg Asp Ala Lys			
100	340	345	350	
102	Asn Leu Ile Glu Gln Leu Glu Gln Asp Lys Gly Met Val Ile Ala Glu			
103	355	360	365	
105	Thr Lys Arg Gln Met His Glu Thr Leu Glu Met Lys Glu Glu Glu Ile			
106	370	375	380	
108	Ala Gln Leu Arg Ser Arg Ile Lys Gln Met Thr Thr Gln Gly Glu Glu			
109	385	390	395	400
111	Leu Arg Glu Gln Lys Glu Lys Ser Glu Arg Ala Ala Phe Glu Glu Leu			
112	405	410	415	
114	Glu Lys Ala Leu Ser Thr Ala Gln Lys Thr Glu Glu Ala Arg Arg Lys			
115	420	425	430	
117	Leu Lys Ala Glu Met Asp Glu Gln Ile Lys Thr Ile Glu Lys Thr Ser			
118	435	440	445	
120	Glu Glu Glu Arg Ile Ser Leu Gln Gln Glu Leu Ser Arg Val Lys Gln			
121	450	455	460	
123	Glu Val Val Asp Val Met Lys Lys Ser Ser Glu Glu Gln Ile Ala Lys			
124	465	470	475	480
126	Leu Gln Lys Leu His Glu Lys Glu Leu Ala Arg Lys Glu Gln Glu Leu			
127	485	490	495	
129	Thr Lys Lys Leu Gln Thr Arg Glu Arg Glu Phe Gln Glu Gln Met Lys			
130	500	505	510	
132	Val Ala Leu Glu Lys Ser Gln Ser Glu Tyr Leu Lys Ile Ser Gln Glu			
133	515	520	525	
135	Lys Glu Gln Gln Glu Ser Leu Ala Leu Glu Glu Leu Glu Leu Gln Lys			
136	530	535	540	
138	Lys Ala Ile Leu Thr Glu Ser Glu Asn Lys Leu Arg Asp Leu Gln Gln			
139	545	550	555	560

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141 Glu Ala Glu Thr Tyr Arg Thr Arg Ile Leu Glu Leu Glu Ser Ser Leu  
 142 565 570 575  
 144 Glu Lys Ser Leu Gln Glu Asn Lys Asn Gln Ser Lys Asp Leu Ala Val  
 145 580 585 590  
 147 His Leu Glu Ala Glu Lys Asn Lys His Asn Lys Glu Ile Thr Val Met  
 148 595 600 605  
 150 Val Glu Lys His Lys Thr Glu Leu Glu Ser Leu Lys His Gln Gln Asp  
 151 610 615 620  
 153 Ala Leu Trp Thr Glu Lys Leu Gln Val Leu Lys Gln Gln Tyr Gln Thr  
 154 625 630 635 640  
 156 Glu Met Glu Lys Leu Arg Glu Lys Cys Glu Gln Glu Lys Glu Thr Leu  
 157 645 650 655  
 159 Leu Lys Asp Lys Glu Ile Ile Phe Gln Ala His Ile Glu Glu Met Asn  
 160 660 665 670  
 162 Glu Lys Thr Leu Glu Lys Leu Asp Val Lys Gln Thr Glu Leu Glu Ser  
 163 675 680 685  
 165 Leu Ser Ser Glu Leu Ser Glu Val Leu Lys Ala Arg His Lys Leu Glu  
 166 690 695 700  
 168 Glu Glu Leu Ser Val Leu Lys Asp Gln Thr Asp Lys Met Lys Gln Glu  
 169 705 710 715 720  
 171 Leu Glu Ala Lys Met Asp Glu Gln Lys Asn His His Gln Gln Val  
 172 725 730 735  
 174 Asp Ser Ile Ile Lys Glu His Glu Val Ser Ile Gln Arg Thr Glu Lys  
 175 740 745 750  
 177 Ala Leu Lys Asp Gln Ile Asn Gln Leu Glu Leu Leu Lys Glu Arg  
 178 755 760 765  
 180 Asp Lys His Leu Lys Glu His Gln Ala His Val Glu Asn Leu Glu Ala  
 181 770 775 780  
 183 Asp Ile Lys Arg Ser Glu Gly Glu Leu Gln Gln Ala Ser Ala Lys Leu  
 184 785 790 795 800  
 186 Asp Val Phe Gln Ser Tyr Gln Ser Ala Thr His Glu Gln Thr Lys Ala  
 187 805 810 815  
 189 Tyr Glu Glu Gln Leu Ala Gln Leu Gln Gln Lys Leu Leu Asp Leu Glu  
 190 820 825 830  
 192 Thr Glu Arg Ile Leu Leu Thr Lys Gln Val Ala Glu Val Glu Ala Gln  
 193 835 840 845  
 195 Lys Lys Asp Val Cys Thr Glu Leu Asp Ala His Lys Ile Gln Val Gln  
 196 850 855 860  
 198 Asp Leu Met Gln Gln Leu Glu Lys Gln Asn Ser Glu Met Glu Gln Lys  
 199 865 870 875 880  
 201 Val Lys Ser Leu Thr Gln Val Tyr Glu Ser Lys Leu Glu Asp Gly Asn  
 202 885 890 895  
 204 Lys Glu Gln Glu Gln Thr Lys Gln Ile Leu Val Glu Lys Glu Asn Met  
 205 900 905 910  
 207 Ile Leu Gln Met Arg Glu Gly Gln Lys Lys Glu Ile Glu Ile Leu Thr  
 208 915 920 925  
 210 Gln Lys Leu Ser Ala Lys Glu Asp Ser Ile His Ile Leu Asn Glu Glu  
 211 930 935 940  
 213 Tyr Glu Thr Lys Phe Lys Asn Gln Glu Lys Lys Met Glu Lys Val Lys

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214	945	950	955	960												
216	Gln	Lys	Ala	Lys	Glu	Met	Gln	Glu	Thr	Leu	Lys	Lys	Leu	Leu	Asp	
217					965				970					975		
219	Gln	Glu	Ala	Lys	Leu	Lys	Lys	Glu	Leu	Glu	Asn	Thr	Ala	Leu	Glu	Leu
220					980				985					990		
222	Ser	Gln	Lys	Glu	Lys	Gln	Phe	Asn	Ala	Lys	Met	Leu	Glu	Met	Ala	Gln
223					995				1000					1005		
225	Ala	Asn	Ser	Ala	Gly	Ile	Ser	Asp	Ala	Val	Ser	Arg	Leu	Glu	Thr	Asn
226					1010			1015				1020				
228	Gln	Lys	Glu	Gln	Ile	Glu	Ser	Leu	Thr	Glu	Val	His	Arg	Arg	Glu	Leu
229	1025				1030				1035					1040		
231	Asn	Asp	Val	Ile	Ser	Ile	Trp	Glu	Lys	Leu	Asn	Gln	Gln	Ala	Glu	
232					1045				1050					1055		
234	Glu	Leu	Gln	Glu	Ile	His	Glu	Ile	Gln	Leu	Gln	Glu	Lys	Glu	Gln	Glu
235					1060				1065					1070		
237	Val	Ala	Glu	Leu	Lys	Gln	Lys	Ile	Leu	Leu	Phe	Gly	Cys	Glu	Lys	Glu
238					1075			1080				1085				
240	Glu	Met	Asn	Lys	Glu	Ile	Thr	Trp	Leu	Lys	Glu	Glu	Gly	Val	Lys	Gln
241					1090			1095				1100				
243	Asp	Thr	Thr	Leu	Asn	Glu	Leu	Gln	Glu	Gln	Leu	Lys	Gln	Lys	Ser	Ala
244	1105				1110				1115					1120		
246	His	Val	Asn	Ser	Leu	Ala	Gln	Asp	Glu	Thr	Lys	Leu	Lys	Ala	His	Leu
247					1125				1130					1135		
249	Glu	Lys	Leu	Glu	Val	Asp	Leu	Asn	Lys	Ser	Leu	Lys	Glu	Asn	Thr	Phe
250					1140				1145					1150		
252	Leu	Gln	Glu	Gln	Leu	Val	Glu	Leu	Lys	Met	Leu	Ala	Glu	Glu	Asp	Lys
253					1155			1160					1165			
255	Arg	Lys	Val	Ser	Glu	Leu	Thr	Ser	Lys	Leu	Lys	Thr	Thr	Asp	Glu	Glu
256					1170			1175				1180				
258	Phe	Gln	Ser	Leu	Lys	Ser	Ser	His	Glu	Lys	Ser	Asn	Lys	Ser	Leu	Glu
259	1185				1190				1195					1200		
261	Asp	Lys	Ser	Leu	Glu	Phe	Lys	Lys	Leu	Ser	Glu	Glu	Leu	Ala	Ile	Gln
262					1205				1210					1215		
264	Leu	Asp	Ile	Cys	Cys	Lys	Lys	Thr	Glu	Ala	Leu	Leu	Glu	Ala	Lys	Thr
265					1220				1225					1230		
267	Asn	Glu	Leu	Ile	Asn	Ile	Ser	Ser	Ser	Lys	Thr	Asn	Ala	Ile	Leu	Ser
268					1235			1240				1245				
270	Arg	Ile	Ser	His	Cys	Gln	His	Arg	Thr	Thr	Lys	Val	Lys	Glu	Ala	Leu
271					1250			1255				1260				
273	Leu	Ile	Lys	Thr	Cys	Thr	Val	Ser	Glu	Leu	Glu	Ala	Gln	Leu	Arg	Gln
274	1265				1270				1275					1280		
276	Leu	Thr	Glu	Glu	Gln	Asn	Thr	Leu	Asn	Ile	Ser	Phe	Gln	Gln	Ala	Thr
277					1285				1290					1295		
279	His	Gln	Leu	Glu	Glu	Lys	Glu	Asn	Gln	Ile	Lys	Ser	Met	Lys	Ala	Asp
280					1300				1305					1310		
282	Ile	Glu	Ser	Leu	Val	Thr	Glu	Lys	Glu	Ala	Leu	Gln	Lys	Glu	Gly	Gly
283					1315			1320				1325				
285	Asn	Gln	Gln	Gln	Ala	Ala	Ser	Glu	Lys	Glu	Ser	Cys	Ile	Thr	Gln	Leu
286					1330			1335				1340				

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288 Lys Lys Glu Leu Ser Glu Asn Ile Asn Ala Val Thr Leu Met Lys Glu  
289 1345 1350 1355 1360  
291 Glu Leu Lys Glu Lys Lys Val Glu Ile Ser Ser Leu Ser Lys Gln Leu  
292 1365 1370 1375  
294 Thr Asp Leu Asn Val Gln Leu Gln Asn Ser Ile Ser Leu Ser Glu Lys  
295 1380 1385 1390  
297 Glu Ala Ala Ile Ser Ser Leu Arg Lys Gln Tyr Asp Glu Glu Lys Cys  
298 1395 1400 1405  
300 Glu Leu Leu Asp Gln Val Gln Asp Leu Ser Phe Lys Val Asp Thr Leu  
301 1410 1415 1420  
303 Ser Lys Glu Lys Ile Ser Ala Leu Glu Gln Val Asp Asp Trp Ser Asn  
304 1425 1430 1435 1440  
306 Lys Phe Ser Glu Trp Lys Lys Ala Gln Ser Arg Phe Thr Gln His  
307 1445 1450 1455  
309 Gln Asn Thr Val Lys Glu Leu Gln Ile Gln Leu Glu Leu Lys Ser Lys  
310 1460 1465 1470  
312 Glu Ala Tyr Glu Lys Asp Glu Gln Ile Asn Leu Leu Lys Glu Glu Leu  
313 1475 1480 1485  
315 Asp Gln Gln Asn Lys Arg Phe Asp Cys Leu Lys Gly Glu Met Glu Asp  
316 1490 1495 1500  
318 Asp Lys Ser Lys Met Glu Lys Lys Glu Ser Asn Leu Glu Thr Glu Leu  
319 1505 1510 1515 1520  
321 Lys Ser Gln Thr Ala Arg Ile Met Glu Leu Glu Asp His Ile Thr Gln  
322 1525 1530 1535  
324 Lys Thr Ile Glu Ile Glu Ser Leu Asn Glu Val Leu Lys Asn Tyr Asn  
325 1540 1545 1550  
327 Gln Gln Lys Asp Ile Glu His Lys Glu Leu Val Gln Lys Leu Gln His  
328 1555 1560 1565  
330 Phe Gln Glu Leu Gly Glu Lys Asp Asn Arg Val Lys Glu Ala Glu  
331 1570 1575 1580  
333 Glu Lys Ile Leu Thr Leu Glu Asn Gln Val Tyr Ser Met Lys Ala Glu  
334 1585 1590 1595 1600  
336 Leu Glu Thr Lys Lys Glu Leu Glu His Val Asn Leu Ser Val Lys  
337 1605 1610 1615  
339 Ser Lys Glu Glu Leu Lys Ala Leu Glu Asp Arg Leu Glu Ser Glu  
340 1620 1625 1630  
342 Ser Ala Ala Lys Leu Ala Glu Leu Lys Arg Lys Ala Glu Gln Lys Ile  
343 1635 1640 1645  
345 Ala Ala Ile Lys Lys Gln Leu Leu Ser Gln Met Glu Glu Lys Glu Glu  
346 1650 1655 1660  
348 Gln Tyr Lys Lys Gly Thr Glu Ser His Leu Ser Glu Leu Asn Thr Lys  
349 1665 1670 1675 1680  
351 Leu Gln Glu Arg Glu Arg Glu Val His Ile Leu Glu Glu Lys Leu Lys  
352 1685 1690 1695  
354 Ser Val Glu Ser Ser Gln Ser Glu Thr Leu Ile Val Pro Arg Ser Ala  
355 1700 1705 1710  
357 Lys Asn Val Ala Ala Tyr Thr Glu Gln Glu Ala Asp Ser Gln Gly  
358 1715 1720 1725  
360 Cys Val Gln Lys Thr Tyr Glu Glu Lys Ile Ser Val Leu Gln Arg Asn

**VERIFICATION SUMMARY**  
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L:10 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date